

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Azko Nobel N.V.
- (B) STREET: Velperweg 76
- 10 (C) CITY: Arnhem
- (E) COUNTRY: The Netherlands
- (F) POSTAL CODE (ZIP): 6824 BM
- (G) TELEPHONE: 0412 666379
- (H) TELEFAX: 0412 650592

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(ii) TITLE OF INVENTION: Recombinant birnavirus vaccine

(iii) NUMBER OF SEQUENCES: 8

20 (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 2827 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- 40 (B) LOCATION: 112..2745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

45 GGATACGATG GGTCTGACCC TCTGGGAGTC ACGAATTAAC GTGGCTACTA GGGGCGATAC

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	CCGCCGCTGG CCGCCACGTT AGTGGCTCCT CTTCTTGATG ATTCTGCCAC C ATG AGT	117
	Met Ser	
	1	
5	GAC ATT TTC AAC AGT CCA CAG GCG CGA AGC ACG ATC TCA GCA GCG TTC	165
	Asp Ile Phe Asn Ser Pro Gln Ala Arg Ser Thr Ile Ser Ala Ala Phe	
	5 10 15	
10	GGC ATA AAG CCT ACT GCT GGA CAA GAC GTG GAA GAA CTC TTG ATC CCT	213
	Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu Ile Pro	
	20 25 30	
15	AAA GTT TGG GTG CCA CCT GAG GAT CCG CTT GCC AGC CCT AGT CGA CTG	261
	Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser Arg Leu	
	35 40 45 50	
20	GCA AAG TTC CTC AGA GAG AAC GGC TAC AAA GTT TTG CAG CCA CGG TCT	309
	Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Val Leu Gln Pro Arg Ser	
	55 60 65	
25	CTG CCC GAG AAT GAG GAG TAT GAG ACC GAC CAA ATA CTC CCA GAC TTA	357
	Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro Asp Leu	
	70 75 80	
30	GCA TGG ATG CGA CAG ATA GAA GGG GCT GTT TTA AAA CCC ACT CTA TCT	405
	Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr Leu Ser	
	85 90 95	
35	CTC CCT ATT GGA GAT CAG GAG TAC TTC CCA AAG TAC TAC CCA ACA CAT	453
	Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro Thr His	
	100 105 110	
40	CGC CCT AGC AAG GAG AAG CCC AAT GCG TAC CCG CCA GAC ATC GCA CTA	501
	Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile Ala Leu	
	115 120 125 130	
45	CTC AAG CAG ATG ATT TAC CTG TTT CTC CAG GTT CCA GAG GCC AAC GAG	549
	Leu Lys Gln Met Ile Tyr Leu Phe Leu Gln Val Pro Glu Ala Asn Glu	
	135 140 145	
50	GGC CTA AAG GAT GAA GTA ACC CTC TTG ACC CAA AAC ATA AGG GAC AAG	597
	Gly Leu Lys Asp Glu Val Thr Leu Leu Thr Gln Asn Ile Arg Asp Lys	
	150 155 160	
55	GCC TAT GGA AGT GGG ACC TAC ATG GGA CAA GCA AAT CGA CTT GTG GCC	645
	Ala Tyr Gly Ser Gly Thr Tyr Met Gly Gln Ala Asn Arg Leu Val Ala	
	165 170 175	

	ATG AAG GAG GTC GCC ACT GGA AGA AAC CCA AAC AAG GAT CCT CTA AAG	693
	Met Lys Glu Val Ala Thr Gly Arg Asn Pro Asn Lys Asp Pro Leu Lys	
	180 185 190	
5	CTT GGG TAC ACT TTT GAG AGC ATC GCG CAG CTA CTT GAC ATC ACA CTA	741
	Leu Gly Tyr Thr Phe Glu Ser Ile Ala Gln Leu Leu Asp Ile Thr Leu	
	195 200 205 210	
10	CCG GTA GGC CCA CCC GGT GAG GAT GAC AAG CCC TGG GTG CCA CTC ACA	789
	Pro Val Gly Pro Pro Gly Glu Asp Asp Lys Pro Trp Val Pro Leu Thr	
	215 220 225	
15	AGA GTG CCG TCA CGG ATG TTG GTG CTG ACG GGA GAC GTA GAT GGC GAC	837
	Arg Val Pro Ser Arg Met Leu Val Leu Thr Gly Asp Val Asp Gly Asp	
	230 235 240	
20	TTT GAG GTT GAA GAT TAC CTT CCC AAA ATC AAC CTC AAG TCA TCA AGT	885
	Phe Glu Val Glu Asp Tyr Leu Pro Lys Ile Asn Leu Lys Ser Ser Ser	
	245 250 255	
	GGA CTA CCA TAT GTA GGT CGC ACC AAA GGA GAG ACA ATT GGC GAG ATG	933
	Gly Leu Pro Tyr Val Gly Arg Thr Lys Gly Glu Thr Ile Gly Glu Met	
	260 265 270	
25	ATA GCT ATC TCA AAC CAG TTT CTC AGA GAG CTA TCA ACA CTG TTG AAG	981
	Ile Ala Ile Ser Asn Gln Phe Leu Arg Glu Leu Ser Thr Leu Leu Lys	
	275 280 285 290	
30	CAA GGT GCA GGG ACA AAG GGG TCA AAC AAG AAG AAG CTA CTC AGC ATG	1029
	Gln Gly Ala Gly Thr Lys Gly Ser Asn Lys Lys Lys Leu Leu Ser Met	
	295 300 305	
35	TTA AGT GAC TAT TGG TAC TTA TCA TGC GGG CTT TTG TTT CCA AAG GCT	1077
	Leu Ser Asp Tyr Trp Tyr Leu Ser Cys Gly Leu Leu Phe Pro Lys Ala	
	310 315 320	
40	GAA AGG TAC GAC AAA AGT ACA TGG CTC ACC AAG ACC CGG AAC ATA TGG	1125
	Glu Arg Tyr Asp Lys Ser Thr Trp Leu Thr Lys Thr Arg Asn Ile Trp	
	325 330 335	
	TCA GCT CCA TCC CCA ACA CAC CTC ATG ATC TCT ATG ATC ACC TGG CCC	1173
	Ser Ala Pro Ser Pro Thr His Leu Met Ile Ser Met Ile Thr Trp Pro	
	340 345 350	
45	GTG ATG TCC AAC AGC CCA AAT AAC GTG TTG AAC ATT GAA GGG TGT CCA	1221
	Val Met Ser Asn Ser Pro Asn Asn Val Leu Asn Ile Glu Gly Cys Pro	
	355 360 365 370	

	TCA CTC TAC AAA TTC AAC CCG TTC AGA GGA GGG TTG AAC AGG ATC GTC	1269
	Ser Leu Tyr Lys Phe Asn Pro Phe Arg Gly Gly Leu Asn Arg Ile Val	
	375 380 385	
5	GAG TGG ATA TTG GCC CCG GAA GAA CCC AAG GCT CTT GTA TAT GCG GAC	1317
	Glu Trp Ile Leu Ala Pro Glu Glu Pro Lys Ala Leu Val Tyr Ala Asp	
	390 395 400	
10	AAC ATA TAC ATT GTC CAC TCA AAC ACG TGG TAC TCA ATT GAC CTA GAG	1365
	Asn Ile Tyr Ile Val His Ser Asn Thr Trp Tyr Ser Ile Asp Leu Glu	
	405 410 415	
15	AAG GGT GAG GCA AAC TGC ACT CGC CAA CAC ATG CAA GCC GCA ATG TAC	1413
	Lys Gly Glu Ala Asn Cys Thr Arg Gln His Met Gln Ala Ala Met Tyr	
	420 425 430	
20	TAC ATA CTC ACC AGA GGG TGG TCA GAC AAC GGC GAC CCA ATG TTC AAT	1461
	Tyr Ile Leu Thr Arg Gly Trp Ser Asp Asn Gly Asp Pro Met Phe Asn	
	435 440 445 450	
	CAA ACA TGG GCC ACC TTT GCC ATG AAC ATT GCC CCT GCT CTA GTG GTG	1509
	Gln Thr Trp Ala Thr Phe Ala Met Asn Ile Ala Pro Ala Leu Val Val	
	455 460 465	
25	GAC TCA TCG TGC CTG ATA ATG AAC CTG CAA ATT AAG ACC TAT GGT CAA	1557
	Asp Ser Ser Cys Leu Ile Met Asn Leu Gln Ile Lys Thr Tyr Gly Gln	
	470 475 480	
30	GGC AGC GGG AAT GCA GCC ACG TTC ATC AAC AAC CAC CTC TTG AGC ACA	1605
	Gly Ser Gly Asn Ala Ala Thr Phe Ile Asn Asn His Leu Leu Ser Thr	
	485 490 495	
35	CTA GTG CTT GAC CAG TGG AAC CTG ATG AGA CAG CCC AGA CCA GAC AGC	1653
	Leu Val Leu Asp Gln Trp Asn Leu Met Arg Gln Pro Arg Pro Asp Ser	
	500 505 510	
40	GAG GAG TTC AAA TCA ATT GAG GAC AAG CTA GGT ATC AAC TTT AAG ATT	1701
	Glu Glu Phe Lys Ser Ile Glu Asp Lys Leu Gly Ile Asn Phe Lys Ile	
	515 520 525 530	
	GAG AGG TCC ATT GAT GAT ATC AGG GGC AAG CTG AGA CAG CTT GTC CTC	1749
	Glu Arg Ser Ile Asp Asp Ile Arg Gly Lys Leu Arg Gln Leu Val Leu	
	535 540 545	
45	CTT GCA CAA CCA GGG TAC CTG AGT GGG GGG GTT GAA CCA GAA CAA TCC	1797
	Leu Ala Gln Pro Gly Tyr Leu Ser Gly Gly Val Glu Pro Glu Gln Ser	
	550 555 560	

	AGC CCA ACT GTT GAG CTT GAC CTA CTA GGG TGG TCA GCT ACA TAC AGC	1845
	Ser Pro Thr Val Glu Leu Asp Leu Leu Gly Trp Ser Ala Thr Tyr Ser	
	565 570 575	
5	AAA GAT CTC GGG ATC TAT GTG CCG GTG CTT GAC AAG GAA CGC CTA TTT	1893
	Lys Asp Leu Gly Ile Tyr Val Pro Val Leu Asp Lys Glu Arg Leu Phe	
	580 585 590	
10	TGT TCT GCT GCG TAT CCC AAG GGA GTA GAG AAC AAG AGT CTC AAG TCC	1941
	Cys Ser Ala Ala Tyr Pro Lys Gly Val Glu Asn Lys Ser Leu Lys Ser	
	595 600 605 610	
15	AAA GTC GGG ATC GAG CAG GCA TAC AAG GTA GTC AGG TAT GAG GCG TTG	1989
	Lys Val Gly Ile Glu Gln Ala Tyr Lys Val Val Arg Tyr Glu Ala Leu	
	615 620 625	
20	AGG TTG GTA GGT GGT TGG AAC TAC CCA CTC CTG AAC AAA GCC TGC AAG	2037
	Arg Leu Val Gly Gly Trp Asn Tyr Pro Leu Leu Asn Lys Ala Cys Lys	
	630 635 640	
25	AAT AAC GCA GGC GCC GCT CGG CGG CAT CTG GAG GCC AAG GGG TTC CCA	2085
	Asn Asn Ala Gly Ala Ala Arg Arg His Leu Glu Ala Lys Gly Phe Pro	
	645 650 655	
30	CTC GAC GAG TTC CTA GCC GAG TGG TCT GAG CTG TCA GAG TTC GGT GAG	2133
	Leu Asp Glu Phe Leu Ala Glu Trp Ser Glu Leu Ser Glu Phe Gly Glu	
	660 665 670	
35	GCC TTC GAA GGC TTC AAT ATC AAG CTG ACC GTA ACA TCT GAG AGC CTA	2181
	Ala Phe Glu Gly Phe Asn Ile Lys Leu Thr Val Thr Ser Glu Ser Leu	
	675 680 685 690	
40	GCC GAA CTG AAC AAG CCA GTA CCC CCC AAG CCC CCA AAT GTC AAC AGA	2229
	Ala Glu Leu Asn Lys Pro Val Pro Pro Lys Pro Pro Asn Val Asn Arg	
	695 700 705	
45	CCA GTC AAC ACT GGG GGA CTC AAG GCA GTC AGC AAC GCC CTC AAG ACC	2277
	Pro Val Asn Thr Gly Gly Leu Lys Ala Val Ser Asn Ala Leu Lys Thr	
	710 715 720	
50	GGT CGG TAC AGG AAC GAA GCC GGA CTG AGT GGT CTC GTC CTT CTA GCC	2325
	Gly Arg Tyr Arg Asn Glu Ala Gly Leu Ser Gly Leu Val Leu Leu Ala	
	725 730 735	
55	ACA GCA AGA AGC CGT CTG CAA GAT GCA GTT AAG GCC AAG GCA GAA GCC	2373
	Thr Ala Arg Ser Arg Leu Gln Asp Ala Val Lys Ala Lys Ala Glu Ala	
	740 745 750	

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 878 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

	Met	Ser	Asp	Ile	Phe	Asn	Ser	Pro	Gln	Ala	Arg	Ser	Thr	Ile	Ser	Ala	
	1				5					10					15		
5	Ala	Phe	Gly	Ile	Lys	Pro	Thr	Ala	Gly	Gln	Asp	Val	Glu	Glu	Leu	Leu	
				20					25					30			
	Ile	Pro	Lys	Val	Trp	Val	Pro	Pro	Glu	Asp	Pro	Leu	Ala	Ser	Pro	Ser	
			35					40						45			
10	Arg	Leu	Ala	Lys	Phe	Leu	Arg	Glu	Asn	Gly	Tyr	Lys	Val	Leu	Gln	Pro	
		50					55					60					
	Arg	Ser	Leu	Pro	Glu	Asn	Glu	Glu	Tyr	Glu	Thr	Asp	Gln	Ile	Leu	Pro	
	65					70					75				80		
15	Asp	Leu	Ala	Trp	Met	Arg	Gln	Ile	Glu	Gly	Ala	Val	Leu	Lys	Pro	Thr	
					85					90					95		
	Leu	Ser	Leu	Pro	Ile	Gly	Asp	Gln	Glu	Tyr	Phe	Pro	Lys	Tyr	Tyr	Pro	
20				100					105					110			
	Thr	His	Arg	Pro	Ser	Lys	Glu	Lys	Pro	Asn	Ala	Tyr	Pro	Pro	Asp	Ile	
			115					120						125			
25	Ala	Leu	Leu	Lys	Gln	Met	Ile	Tyr	Leu	Phe	Leu	Gln	Val	Pro	Glu	Ala	
		130				135						140					
	Asn	Glu	Gly	Leu	Lys	Asp	Glu	Val	Thr	Leu	Leu	Thr	Gln	Asn	Ile	Arg	
	145				150						155				160		
30	Asp	Lys	Ala	Tyr	Gly	Ser	Gly	Thr	Tyr	Met	Gly	Gln	Ala	Asn	Arg	Leu	
				165					170					175			
	Val	Ala	Met	Lys	Glu	Val	Ala	Thr	Gly	Arg	Asn	Pro	Asn	Lys	Asp	Pro	
35				180					185					190			
	Leu	Lys	Leu	Gly	Tyr	Thr	Phe	Glu	Ser	Ile	Ala	Gln	Leu	Leu	Asp	Ile	
			195				200						205				
40	Thr	Leu	Pro	Val	Gly	Pro	Pro	Gly	Glu	Asp	Asp	Lys	Pro	Trp	Val	Pro	
		210					215						220				
	Leu	Thr	Arg	Val	Pro	Ser	Arg	Met	Leu	Val	Leu	Thr	Gly	Asp	Val	Asp	
	225				230						235				240		
45	Gly	Asp	Phe	Glu	Val	Glu	Asp	Tyr	Leu	Pro	Lys	Ile	Asn	Leu	Lys	Ser	
				245						250					255		

	Ser Ser Gly Leu Pro Tyr Val Gly Arg Thr Lys Gly Glu Thr Ile Gly	
	260	265 270
5	Glu Met Ile Ala Ile Ser Asn Gln Phe Leu Arg Glu Leu Ser Thr Leu	
	275	280 285
	Leu Lys Gln Gly Ala Gly Thr Lys Gly Ser Asn Lys Lys Lys Leu Leu	
	290	295 300
10	Ser Met Leu Ser Asp Tyr Trp Tyr Leu Ser Cys Gly Leu Leu Phe Pro	
	305	310 315 320
	Lys Ala Glu Arg Tyr Asp Lys Ser Thr Trp Leu Thr Lys Thr Arg Asn	
	325	330 335
15	Ile Trp Ser Ala Pro Ser Pro Thr His Leu Met Ile Ser Met Ile Thr	
	340	345 350
20	Trp Pro Val Met Ser Asn Ser Pro Asn Asn Val Leu Asn Ile Glu Gly	
	355	360 365
	Cys Pro Ser Leu Tyr Lys Phe Asn Pro Phe Arg Gly Gly Leu Asn Arg	
	370	375 380
25	Ile Val Glu Trp Ile Leu Ala Pro Glu Glu Pro Lys Ala Leu Val Tyr	
	385	390 395 400
	Ala Asp Asn Ile Tyr Ile Val His Ser Asn Thr Trp Tyr Ser Ile Asp	
	405	410 415
30	Leu Glu Lys Gly Glu Ala Asn Cys Thr Arg Gln His Met Gln Ala Ala	
	420	425 430
35	Met Tyr Tyr Ile Leu Thr Arg Gly Trp Ser Asp Asn Gly Asp Pro Met	
	435	440 445
	Phe Asn Gln Thr Trp Ala Thr Phe Ala Met Asn Ile Ala Pro Ala Leu	
	450	455 460
40	Val Val Asp Ser Ser Cys Leu Ile Met Asn Leu Gln Ile Lys Thr Tyr	
	465	470 475 480
	Gly Gln Gly Ser Gly Asn Ala Ala Thr Phe Ile Asn Asn His Leu Leu	
	485	490 495
45	Ser Thr Leu Val Leu Asp Gln Trp Asn Leu Met Arg Gln Pro Arg Pro	
	500	505 510

Asp Ser Glu Glu Phe Lys Ser Ile Glu Asp Lys Leu Gly Ile Asn Phe
 515 520 525

5 Lys Ile Glu Arg Ser Ile Asp Asp Ile Arg Gly Lys Leu Arg Gln Leu
 530 535 540

Val Leu Leu Ala Gln Pro Gly Tyr Leu Ser Gly Gly Val Glu Pro Glu
 545 550 555 560

10 Gln Ser Ser Pro Thr Val Glu Leu Asp Leu Leu Gly Trp Ser Ala Thr
 565 570 575

Tyr Ser Lys Asp Leu Gly Ile Tyr Val Pro Val Leu Asp Lys Glu Arg
 580 585 590

15 Leu Phe Cys Ser Ala Ala Tyr Pro Lys Gly Val Glu Asn Lys Ser Leu
 595 600 605

20 Lys Ser Lys Val Gly Ile Glu Gln Ala Tyr Lys Val Val Arg Tyr Glu
 610 615 620

Ala Leu Arg Leu Val Gly Gly Trp Asn Tyr Pro Leu Leu Asn Lys Ala
 625 630 635 640

25 Cys Lys Asn Asn Ala Gly Ala Ala Arg Arg His Leu Glu Ala Lys Gly
 645 650 655

Phe Pro Leu Asp Glu Phe Leu Ala Glu Trp Ser Glu Leu Ser Glu Phe
 660 665 670

30 Gly Glu Ala Phe Glu Gly Phe Asn Ile Lys Leu Thr Val Thr Ser Glu
 675 680 685

35 Ser Leu Ala Glu Leu Asn Lys Pro Val Pro Pro Lys Pro Pro Asn Val
 690 695 700

Asn Arg Pro Val Asn Thr Gly Gly Leu Lys Ala Val Ser Asn Ala Leu
 705 710 715 720

40 Lys Thr Gly Arg Tyr Arg Asn Glu Ala Gly Leu Ser Gly Leu Val Leu
 725 730 735

Leu Ala Thr Ala Arg Ser Arg Leu Gln Asp Ala Val Lys Ala Lys Ala
 740 745 750

45 Glu Ala Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp
 755 760 765

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Trp Phe Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp
  770                      775                      780

Ile Ala Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala
5  785                      790                      795                      800

Leu Glu Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu
                      805                      810                      815

10 Val Lys Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu
                      820                      825                      830

Pro Ala Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly
                      835                      840                      845

15 Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala
                      850                      855                      860

Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg
20 865                      870                      875

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(2) INFORMATION FOR SEQ ID NO: 3:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: cDNA

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- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 97..531

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GGATACGATC GGTCTGACCC CGGGGGAGTC ACCCGGGGAC AGGCCGTCAA GGCCTTGTTTC 60

CAGGATGGGA CTCCTCCTTC TACAACGCTA TCATTG ATG GTT AGT AGA GAT CAG 114

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Met Val Ser Arg Asp Gln

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	ACA AAC GAT CGC AGC GAT GAC AAA CCT GCA AGA TCA AAC CCA ACA GAT	162
	Thr Asn Asp Arg Ser Asp Asp Lys Pro Ala Arg Ser Asn Pro Thr Asp	
	10 15 20	
5	TGT TCC GTT CAT ACG GAG CCT TCT GAT GCC AAC AAC CGG ACC GGC GTC	210
	Cys Ser Val His Thr Glu Pro Ser Asp Ala Asn Asn Arg Thr Gly Val	
	25 30 35	
10	CAT TCC GGA CGA CAC CCT GGA GAA GCA CAC TCT CAG GTC AGA GAC CTC	258
	His Ser Gly Arg His Pro Gly Glu Ala His Ser Gln Val Arg Asp Leu	
	40 45 50	
15	GAC CTA CAA TTT GAC TGT GGG GGA CAC AGG GTC AGG GCT AAT TGT CTT	306
	Asp Leu Gln Phe Asp Cys Gly Gly His Arg Val Arg Ala Asn Cys Leu	
	55 60 65 70	
20	TTT CCC TGG ATT CCC TGG CTC AAT TGT GGG TGC TCA CTA CAC ACT GCA	354
	Phe Pro Trp Ile Pro Trp Leu Asn Cys Gly Cys Ser Leu His Thr Ala	
	75 80 85	
25	GGG CAA TGG GAA CTA CAA GTT CGA TCA GAT GCT CCT GAC TGC CCA GAA	402
	Gly Gln Trp Glu Leu Gln Val Arg Ser Asp Ala Pro Asp Cys Pro Glu	
	90 95 100	
30	CCT ACC GGC CAG TTA CAA CTA CTG CAG GCT AGT GAG TCG GAG TCT CAC	450
	Pro Thr Gly Gln Leu Gln Leu Leu Gln Ala Ser Glu Ser Glu Ser His	
	105 110 115	
35	AGT GAG GTC AAG CAC ACT TCC TGG TGG CGT TTT TGC ACT AAA CGG CAC	498
	Ser Glu Val Lys His Thr Ser Trp Trp Arg Leu Cys Thr Lys Arg His	
	120 125 130	
40	CAT AAA CGC CGT GAC CTT CCA AGG AAG CCT GAG TGA ACT GACA GAT GTTAGCT	551
	His Lys Arg Arg Asp Leu Pro Arg Lys Pro Glu	
	135 140 145	
45	ACAATGGGTT GATGTCTGCA ACAGCCAACA TCAACGACAA AATTGGGAAC GTCCTAGTAG	611
	GGGAAGGGGT CACCGTCCTC AGCTTACCCA CATCATATGA TCTTGGGTAT GTGAGGCTTG	671
	GTGACCCCAT TCCCGCAATA GGGCTTGACC CAAAAATGGT AGCCACATGT GACAGCAGTG	731
	ACAGGCCCAG AGTCTACACC ATA ACTGCAG CCGATGATTA CCAATTCTCA TCACAGTACC	791
	AACCAGGTGG GGTAACAATC AACTGTCTCT CAGCCAACAT TGATGCCATC ACAAGCCTCA	851
	GCGTTGGGGG AGAGCTCGTG TTTCAAACAA GCGTCCACGG CCTTG TACTG GCGCCACCA	911

	TCTACCTCAT	AGGCTTTGAT	GGGACAACGG	TAATCACCAG	GGCTGTGGCC	GCAAACAATG	971
	GGCTGACGAC	CGGCACCGAC	AACCTTATGC	CATTCAATCT	TGTGATTCCA	ACAAACGAGA	1031
5	TAACCCAGCC	AATCACATCC	ATCAAACCTGG	AGATAGTGAC	CTCCAAAAGT	GGTGGTCAGG	1091
	CAGGGGATCA	GATGTCATGG	TCGGCAAGAG	GGAGCCTAGC	AGTGACGATC	CATGGTGGCA	1151
	ACTATCCAGG	GGCCCTCCGT	CCCGTCACGC	TAGTGGCCTA	CGAAAGAGTG	GCAACAGGAT	1211
10	CCGTCGTTAC	GGTCGCTGGG	GTGAGCAACT	TCGAGCTGAT	CCCAAATCCT	GAAGTAGCAA	1271
	AGAACCTGGT	TACAGAATAC	GGCCGATTTG	ACCCAGGAGC	CATGAACTAC	ACAAAATTGA	1331
15	TACTGAGTGA	GAGGGACCGT	CTTGGCATCA	AGACCGTCTG	GCCAACAAGG	GAGTACACTG	1391
	ACTTTCGTGA	ATACTTCATG	GAGGTGGCCG	ACCTCAACTC	TCCCCTGAAG	ATTGCAGGAG	1451
	CATTTCGGCTT	CAAAGACATA	ATCCGGGCCA	TAAGGAGGAT	AGCTGTGCCG	GTGGTCTCCA	1511
20	CATTGTTCCC	ACCTGCCGCT	CCCCTAGCCC	ATGCAATTGG	GGAAGGTGTA	GACTACCTGC	1571
	TGGGCGATGA	GGCACAGGCT	GCTTCAGGAA	CTGCTCGAGC	CGCGTCAGGA	AAAGCAAGAG	1631
25	CTGCCTCAGG	CCGCATAAGG	CAGCTGACTC	TCGCCGCCGA	CAAGGGGTAC	GAGGTAGTCG	1691
	CGAATCTATT	CCAGGTGCCC	CAGAATCCCG	TAGTCGACGG	GATTCTTGCT	TCACCTGGGG	1751
	TACTCCGCGG	TGCACACAAC	CTCGACTGCG	TGTTAAGAGA	GGGTGCCACG	CTATTCCCTG	1811
30	TGGTTATTAC	GACAGTGGAA	GACGCCATGA	CACCCAAAGC	ATTGAACAGC	AAAATGTTTG	1871
	CTGTCATTGA	AGGCGTGCGA	GAAGACCTCC	AACCTCCATC	TCAAAGAGGA	TCCTTCATAC	1931
35	GAACTCTCTC	TGGACACAGA	GTCTATGGAT	ATGCTCCAGA	TGGGGTACTT	CCACTGGAGA	1991
	CTGGGAGAGA	CTACACCGTT	GTCCCAATAG	ATGATGTCTG	GGACGACAGC	ATTATGCTGT	2051
	CCAAAGATCC	CATACCTCCT	ATTGTGGGAA	ACAGTGGAAG	TCTAGCCATA	GCTTACATGG	2111
40	ATGTGTTTCG	ACCCAAAGTC	CCAATCCATG	TGGCTATGAC	GGGAGCCCTC	AATGCTTGTG	2171
	GCGAGATTGA	GAAAGTAAGC	TTTAGAAGCA	CCAAGCTCGC	CACTGCACAC	CGACTTGGCC	2231
45	TTAGGTTGGC	TGGTCCCGGA	GCATTGATG	TAAACACCGG	GCCCAACTGG	GCAACGTTCA	2291
	TCAAACGTTT	CCCTCACAAAT	CCACGCGACT	GGGACAGGCT	CCCCTACCTC	AACCTACCAT	2351

ACCTTCCACC CAATGCAGGA CGCCAGTACC ACCTTGCCAT GGCTGCATCA GAGTTCAAAG 2411
 AGACCCCCGA ACTCGAGAGT GCCGTCAGAG CAATGGAAGC AGCAGCCAAC GTGGACCCAC 2471
 5 TATTCCAATC TGCACTCAGT GTGTTCATGT GGCTGGAAGA GAATGGGATT GTGACTGACA 2531
 TGGCCAACTT CGCACTCAGC GACCCGAACG CCCATCGGAT GCGAAATTTT CTTGCAAACG 2591
 CACCACAAGC AGGCAGCAAG TCGCAAAGGG CCAAGTACGG GACAGCAGGC TACGGAGTGG 2651
 10 AGGCTCGGGG CCCCACACCA GAGGAAGCAC AGAGGGAAAA AGACACACGG ATCTCAAAGA 2711
 AGATGGAGAC CATGGGCATC TACTTTGCAA CACCAGAATG GGTAGCACTC AATGGGCACC 2771
 15 GAGGGCCAAG CCCC GGCCAG CTAAAGTACT GGCAGAACAC ACGAGAAATA CCGGACCCAA 2831
 ACGAGGACTA TCTAGACTAC GTGCATGCAG AGAAGAGCCG GTTGGCATCA GAAGAACAAA 2891
 TCCTAAGGGC AGCTACGTCG ATCTACGGGG CTCCAGGACA GGCAGAGCCA CCCC AAGCTT 2951
 20 TCATAGACGA AGTTGCCAAA GTCTATGAAA TCAACCATGG ACGTGGCCCA AACCAAGAAC 3011
 AGATGAAAGA TCTGCTCTTG ACTGCGATGG AGATGAAGCA TCGCAATCCC AGGCGGGCTC 3071
 25 TACCAAAGCC CAAGCCAAAA CCCAATGCTC CAACACAGAG ACCCCCTGGT CGGCTGGGCC 3131
 GCTGGATCAG GACCGTCTCT GATGAGGACC TTGAGTGAGG CTCCTGGGAG TCTCCCGACA 3191
 CCACCCGCGC AGGTGTGGAC ACCAATTCGG CTTACAACA TCCCAAATTG GATCCGTTTCG 3251
 30 CGGGTCCCCT 3261

35 (2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 145 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

45 Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp Asp Lys Pro Ala
 1 5 10 15

Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu Pro Ser Asp Ala
 20 25 30
 Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro Gly Glu Ala His
 5 35 40 45
 Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys Gly Gly His Arg
 50 55 60
 10 Val Arg Ala Asn Cys Leu Phe Pro Trp Ile Pro Trp Leu Asn Cys Gly
 65 70 75 80
 Cys Ser Leu His Thr Ala Gly Gln Trp Glu Leu Gln Val Arg Ser Asp
 85 90 95
 15 Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln Leu Leu Gln Ala
 100 105 110
 Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr Ser Trp Trp Arg
 20 115 120 125
 Leu Cys Thr Lys Arg His His Lys Arg Arg Asp Leu Pro Arg Lys Pro
 130 135 140
 25 Glu
 145

30 (2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3261 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

40

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION:131..3166

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GGATACGATC GGTCTGACCC CGGGGGAGTC ACCCGGGGAC AGGCCGTCAA GGCCTTG TTC

60

	CAGGATGGGA CTCCTCCTTC TACAACGCTA TCATTGATGG TTAGTAGAGA TCAGACAAAC	120
5	GATCGCAGCG ATG ACA AAC CTG CAA GAT CAA ACC CAA CAG ATT GTT CCG Met Thr Asn Leu Gln Asp Gln Thr Gln Gln Ile Val Pro 1 5 10	169
10	TTC ATA CGG AGC CTT CTG ATG CCA ACA ACC GGA CCG GCG TCC ATT CCG Phe Ile Arg Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro 15 20 25	217
15	GAC GAC ACC CTG GAG AAG CAC ACT CTC AGG TCA GAG ACC TCG ACC TAC Asp Asp Thr Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr 30 35 40 45	265
20	AAT TTG ACT GTG GGG GAC ACA GGG TCA GGG CTA ATT GTC TTT TTC CCT Asn Leu Thr Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro 50 55 60	313
25	GGA TTC CCT GGC TCA ATT GTG GGT GCT CAC TAC ACA CTG CAG GGC AAT Gly Phe Pro Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Gly Asn 65 70 75	361
30	GGG AAC TAC AAG TTC GAT CAG ATG CTC CTG ACT GCC CAG AAC CTA CCG Gly Asn Tyr Lys Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro 80 85 90	409
35	GCC AGT TAC AAC TAC TGC AGG CTA GTG AGT CGG AGT CTC ACA GTG AGG Ala Ser Tyr Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg 95 100 105	457
40	TCA AGC ACA CTT CCT GGT GGC GTT TAT GCA CTA AAC GGC ACC ATA AAC Ser Ser Thr Leu Pro Gly Gly Val Tyr Ala Leu Asn Gly Thr Ile Asn 110 115 120 125	505
45	GCC GTG ACC TTC CAA GGA AGC CTG AGT GAA CTG ACA GAT GTT AGC TAC Ala Val Thr Phe Gln Gly Ser Leu Ser Glu Leu Thr Asp Val Ser Tyr 130 135 140	553
50	AAT GGG TTG ATG TCT GCA ACA GCC AAC ATC AAC GAC AAA ATT GGG AAC Asn Gly Leu Met Ser Ala Thr Ala Asn Ile Asn Asp Lys Ile Gly Asn 145 150 155	601
55	GTC CTA GTA GGG GAA GGG GTC ACC GTC CTC AGC TTA CCC ACA TCA TAT Val Leu Val Gly Glu Gly Val Thr Val Leu Ser Leu Pro Thr Ser Tyr 160 165 170	649
60	GAT CTT GGG TAT GTG AGG CTT GGT GAC CCC ATT CCC GCA ATA GGG CTT	697

	Asp	Leu	Gly	Tyr	Val	Arg	Leu	Gly	Asp	Pro	Ile	Pro	Ala	Ile	Gly	Leu	
	175						180					185					
5	GAC	CCA	AAA	ATG	GTA	GCC	ACA	TGT	GAC	AGC	AGT	GAC	AGG	CCC	AGA	GTC	745
	Asp	Pro	Lys	Met	Val	Ala	Thr	Cys	Asp	Ser	Ser	Asp	Arg	Pro	Arg	Val	
	190					195				200					205		
10	TAC	ACC	ATA	ACT	GCA	GCC	GAT	GAT	TAC	CAA	TTC	TCA	TCA	CAG	TAC	CAA	793
	Tyr	Thr	Ile	Thr	Ala	Ala	Asp	Asp	Tyr	Gln	Phe	Ser	Ser	Gln	Tyr	Gln	
					210				215						220		
15	CCA	GGT	GGG	GTA	ACA	ATC	ACA	CTG	TTC	TCA	GCC	AAC	ATT	GAT	GCC	ATC	841
	Pro	Gly	Gly	Val	Thr	Ile	Thr	Leu	Phe	Ser	Ala	Asn	Ile	Asp	Ala	Ile	
					225				230					235			
	ACA	AGC	CTC	AGC	GTT	GGG	GGA	GAG	CTC	GTG	TTT	CAA	ACA	AGC	GTC	CAC	889
	Thr	Ser	Leu	Ser	Val	Gly	Gly	Glu	Leu	Val	Phe	Gln	Thr	Ser	Val	His	
					240				245					250			
20	GGC	CTT	GTA	CTG	GGC	GCC	ACC	ATC	TAC	CTC	ATA	GGC	TTT	GAT	GGG	ACA	937
	Gly	Leu	Val	Leu	Gly	Ala	Thr	Ile	Tyr	Leu	Ile	Gly	Phe	Asp	Gly	Thr	
					255				260					265			
25	ACG	GTA	ATC	ACC	AGG	GCT	GTG	GCC	GCA	AAC	AAT	GGG	CTG	ACG	ACC	GGC	985
	Thr	Val	Ile	Thr	Arg	Ala	Val	Ala	Ala	Asn	Asn	Gly	Leu	Thr	Thr	Gly	
	270					275					280					285	
30	ACC	GAC	AAC	CTT	ATG	CCA	TTC	AAT	CTT	GTG	ATT	CCA	ACA	AAC	GAG	ATA	1033
	Thr	Asp	Asn	Leu	Met	Pro	Phe	Asn	Leu	Val	Ile	Pro	Thr	Asn	Glu	Ile	
					290					295					300		
35	ACC	CAG	CCA	ATC	ACA	TCC	ATC	AAA	CTG	GAG	ATA	GTG	ACC	TCC	AAA	AGT	1081
	Thr	Gln	Pro	Ile	Thr	Ser	Ile	Lys	Leu	Glu	Ile	Val	Thr	Ser	Lys	Ser	
					305				310					315			
	GGT	GGT	CAG	GCA	GGG	GAT	CAG	ATG	TCA	TGG	TCG	GCA	AGA	GGG	AGC	CTA	1129
	Gly	Gly	Gln	Ala	Gly	Asp	Gln	Met	Ser	Trp	Ser	Ala	Arg	Gly	Ser	Leu	
					320				325					330			
40	GCA	GTG	ACG	ATC	CAT	GGT	GGC	AAC	TAT	CCA	GGG	GCC	CTC	CGT	CCC	GTC	1177
	Ala	Val	Thr	Ile	His	Gly	Gly	Asn	Tyr	Pro	Gly	Ala	Leu	Arg	Pro	Val	
					335				340					345			
45	ACG	CTA	GTG	GCC	TAC	GAA	AGA	GTG	GCA	ACA	GGA	TCC	GTC	GTT	ACG	GTC	1225
	Thr	Leu	Val	Ala	Tyr	Glu	Arg	Val	Ala	Thr	Gly	Ser	Val	Val	Thr	Val	
					350				355					360		365	
	GCT	GGG	GTG	AGC	AAC	TTC	GAG	CTG	ATC	CCA	AAT	CCT	GAA	CTA	GCA	AAG	1273

	Ala Gly Val Ser Asn Phe Glu Leu Ile Pro Asn Pro Glu Leu Ala Lys	
	370 375 380	
5	AAC CTG GTT ACA GAA TAC GGC CGA TTT GAC CCA GGA GCC ATG AAC TAC Asn Leu Val Thr Glu Tyr Gly Arg Phe Asp Pro Gly Ala Met Asn Tyr	1321
	385 390 395	
10	ACA AAA TTG ATA CTG AGT GAG AGG GAC CGT CTT GGC ATC AAG ACC GTC Thr Lys Leu Ile Leu Ser Glu Arg Asp Arg Leu Gly Ile Lys Thr Val	1369
	400 405 410	
15	TGG CCA ACA AGG GAG TAC ACT GAC TTT CGT GAA TAC TTC ATG GAG GTG Trp Pro Thr Arg Glu Tyr Thr Asp Phe Arg Glu Tyr Phe Met Glu Val	1417
	415 420 425	
20	GCC GAC CTC AAC TCT CCC CTG AAG ATT GCA GGA GCA TTC GGC TTC AAA Ala Asp Leu Asn Ser Pro Leu Lys Ile Ala Gly Ala Phe Gly Phe Lys	1465
	430 435 440 445	
25	GAC ATA ATC CGG GCC ATA AGG AGG ATA GCT GTG CCG GTG GTC TCC ACA Asp Ile Ile Arg Ala Ile Arg Arg Ile Ala Val Pro Val Val Ser Thr	1513
	450 455 460	
30	TTG TTC CCA CCT GCC GCT CCC CTA GCC CAT GCA ATT GGG GAA GGT GTA Leu Phe Pro Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val	1561
	465 470 475	
35	GAC TAC CTG CTG GGC GAT GAG GCA CAG GCT GCT TCA GGA ACT GCT CGA Asp Tyr Leu Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg	1609
	480 485 490	
40	GCC GCG TCA GGA AAA GCA AGA GCT GCC TCA GGC CGC ATA AGG CAG CTG Ala Ala Ser Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu	1657
	495 500 505	
45	ACT CTC GCC GCC GAC AAG GGG TAC GAG GTA GTC GCG AAT CTA TTC CAG Thr Leu Ala Ala Asp Lys Gly Tyr Glu Val Val Ala Asn Leu Phe Gln	1705
	510 515 520 525	
50	GTG CCC CAG AAT CCC GTA GTC GAC GGG ATT CTT GCT TCA CCT GGG GTA Val Pro Gln Asn Pro Val Val Asp Gly Ile Leu Ala Ser Pro Gly Val	1753
	530 535 540	
55	CTC CGC GGT GCA CAC AAC CTC GAC TGC GTG TTA AGA GAG GGT GCC ACG Leu Arg Gly Ala His Asn Leu Asp Cys Val Leu Arg Glu Gly Ala Thr	1801
	545 550 555	
	CTA TTC CCT GTG GTT ATT ACG ACA GTG GAA GAC GCC ATG ACA CCC AAA	1849

	Leu Phe Pro Val Val Ile Thr Thr Val Glu Asp Ala Met Thr Pro Lys	
	560 565 570	
5	GCA TTG AAC AGC AAA ATG TTT GCT GTC ATT GAA GGC GTG CGA GAA GAC Ala Leu Asn Ser Lys Met Phe Ala Val Ile Glu Gly Val Arg Glu Asp	1897
	575 580 585	
10	CTC CAA CCT CCA TCT CAA AGA GGA TCC TTC ATA CGA ACT CTC TCT GGA Leu Gln Pro Pro Ser Gln Arg Gly Ser Phe Ile Arg Thr Leu Ser Gly	1945
	590 595 600 605	
15	CAC AGA GTC TAT GGA TAT GCT CCA GAT GGG GTA CTT CCA CTG GAG ACT His Arg Val Tyr Gly Tyr Ala Pro Asp Gly Val Leu Pro Leu Glu Thr	1993
	610 615 620	
	GGG AGA GAC TAC ACC GTT GTC CCA ATA GAT GAT GTC TGG GAC GAC AGC Gly Arg Asp Tyr Thr Val Val Pro Ile Asp Asp Val Trp Asp Asp Ser	2041
	625 630 635	
20	ATT ATG CTG TCC AAA GAT CCC ATA CCT CCT ATT GTG GGA AAC AGT GGA Ile Met Leu Ser Lys Asp Pro Ile Pro Pro Ile Val Gly Asn Ser Gly	2089
	640 645 650	
25	AAT CTA GCC ATA GCT TAC ATG GAT GTG TTT CGA CCC AAA GTC CCA ATC Asn Leu Ala Ile Ala Tyr Met Asp Val Phe Arg Pro Lys Val Pro Ile	2137
	655 660 665	
30	CAT GTG GCT ATG ACG GGA GCC CTC AAT GCT TGT GGC GAG ATT GAG AAA His Val Ala Met Thr Gly Ala Leu Asn Ala Cys Gly Glu Ile Glu Lys	2185
	670 675 680 685	
35	GTA AGC TTT AGA AGC ACC AAG CTC GCC ACT GCA CAC CGA CTT GGC CTT Val Ser Phe Arg Ser Thr Lys Leu Ala Thr Ala His Arg Leu Gly Leu	2233
	690 695 700	
	AGG TTG GCT GGT CCC GGA GCA TTC GAT GTA AAC ACC GGG CCC AAC TGG Arg Leu Ala Gly Pro Gly Ala Phe Asp Val Asn Thr Gly Pro Asn Trp	2281
	705 710 715	
40	GCA ACG TTC ATC AAA CGT TTC CCT CAC AAT CCA CGC GAC TGG GAC AGG Ala Thr Phe Ile Lys Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg	2329
	720 725 730	
45	CTC CCC TAC CTC AAC CTA CCA TAC CTT CCA CCC AAT GCA GGA CGC CAG Leu Pro Tyr Leu Asn Leu Pro Tyr Leu Pro Pro Asn Ala Gly Arg Gln	2377
	735 740 745	
	TAC CAC CTT GCC ATG GCT GCA TCA GAG TTC AAA GAG ACC CCC GAA CTC	2425

	Tyr	His	Leu	Ala	Met	Ala	Ala	Ser	Glu	Phe	Lys	Glu	Thr	Pro	Glu	Leu	
	750					755					760					765	
5	GAG	AGT	GCC	GTC	AGA	GCA	ATG	GAA	GCA	GCA	GCC	AAC	GTG	GAC	CCA	CTA	2473
	Glu	Ser	Ala	Val	Arg	Ala	Met	Glu	Ala	Ala	Ala	Asn	Val	Asp	Pro	Leu	
					770				775						780		
10	TTC	CAA	TCT	GCA	CTC	AGT	GTG	TTC	ATG	TGG	CTG	GAA	GAG	AAT	GGG	ATT	2521
	Phe	Gln	Ser	Ala	Leu	Ser	Val	Phe	Met	Trp	Leu	Glu	Glu	Asn	Gly	Ile	
				785					790						795		
15	GTG	ACT	GAC	ATG	GCC	AAC	TTC	GCA	CTC	AGC	GAC	CCG	AAC	GCC	CAT	CGG	2569
	Val	Thr	Asp	Met	Ala	Asn	Phe	Ala	Leu	Ser	Asp	Pro	Asn	Ala	His	Arg	
			800					805					810				
	ATG	CGA	AAT	TTT	CTT	GCA	AAC	GCA	CCA	CAA	GCA	GGC	AGC	AAG	TCG	CAA	2617
	Met	Arg	Asn	Phe	Leu	Ala	Asn	Ala	Pro	Gln	Ala	Gly	Ser	Lys	Ser	Gln	
		815				820					825						
20	AGG	GCC	AAG	TAC	GGG	ACA	GCA	GGC	TAC	GGA	GTG	GAG	GCT	CGG	GGC	CCC	2665
	Arg	Ala	Lys	Tyr	Gly	Thr	Ala	Gly	Tyr	Gly	Val	Glu	Ala	Arg	Gly	Pro	
	830					835				840					845		
25	ACA	CCA	GAG	GAA	GCA	CAG	AGG	GAA	AAA	GAC	ACA	CGG	ATC	TCA	AAG	AAG	2713
	Thr	Pro	Glu	Glu	Ala	Gln	Arg	Glu	Lys	Asp	Thr	Arg	Ile	Ser	Lys	Lys	
					850					855					860		
30	ATG	GAG	ACC	ATG	GGC	ATC	TAC	TTT	GCA	ACA	CCA	GAA	TGG	GTA	GCA	CTC	2761
	Met	Glu	Thr	Met	Gly	Ile	Tyr	Phe	Ala	Thr	Pro	Glu	Trp	Val	Ala	Leu	
				865					870					875			
35	AAT	GGG	CAC	CGA	GGG	CCA	AGC	CCC	GGC	CAG	CTA	AAG	TAC	TGG	CAG	AAC	2809
	Asn	Gly	His	Arg	Gly	Pro	Ser	Pro	Gly	Gln	Leu	Lys	Tyr	Trp	Gln	Asn	
			880					885					890				
	ACA	CGA	GAA	ATA	CCG	GAC	CCA	AAC	GAG	GAC	TAT	CTA	GAC	TAC	GTG	CAT	2857
	Thr	Arg	Glu	Ile	Pro	Asp	Pro	Asn	Glu	Asp	Tyr	Leu	Asp	Tyr	Val	His	
		895					900					905					
40	GCA	GAG	AAG	AGC	CGG	TTG	GCA	TCA	GAA	GAA	CAA	ATC	CTA	AGG	GCA	GCT	2905
	Ala	Glu	Lys	Ser	Arg	Leu	Ala	Ser	Glu	Glu	Gln	Ile	Leu	Arg	Ala	Ala	
	910					915					920					925	
45	ACG	TCG	ATC	TAC	GGG	GCT	CCA	GGA	CAG	GCA	GAG	CCA	CCC	CAA	GCT	TTC	2953
	Thr	Ser	Ile	Tyr	Gly	Ala	Pro	Gly	Gln	Ala	Glu	Pro	Pro	Gln	Ala	Phe	
					930				935					940			
	ATA	GAC	GAA	GTT	GCC	AAA	GTC	TAT	GAA	ATC	AAC	CAT	GGA	CGT	GGC	CCA	3001

Ile Asp Glu Val Ala Lys Val Tyr Glu Ile Asn His Gly Arg Gly Pro
 945 950 955

5 AAC CAA GAA CAG ATG AAA GAT CTG CTC TTG ACT GCG ATG GAG ATG AAG 3049
 Asn Gln Glu Gln Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys
 960 965 970

10 CAT CGC AAT CCC AGG CGG GCT CTA CCA AAG CCC AAG CCA AAA CCC AAT 3097
 His Arg Asn Pro Arg Arg Ala Leu Pro Lys Pro Lys Pro Lys Pro Asn
 975 980 985

15 GCT CCA ACA CAG AGA CCC CCT GGT CGG CTG GGC CGC TGG ATC AGG ACC 3145
 Ala Pro Thr Gln Arg Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr
 990 995 1000 1005

GTC TCT GAT GAG GAC CTT GAG TGAGGCTCCT GGGAGTCTCC CGACACCACC 3196
 Val Ser Asp Glu Asp Leu Glu
 1010

20 CGCGCAGGTG TGGACACCAA TTCGGCCTTA CAACATCCCA AATTGGATCC GTTCGCGGGT 3256

CCCCT 3261

25

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 1012 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Thr Asn Leu Gln Asp Gln Thr Gln Gln Ile Val Pro Phe Ile Arg
 1 5 10 15

40 Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr
 20 25 30

Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr
 35 40 45

45 Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro
 50 55 60

Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Gly Asn Gly Asn Tyr

	65		70		75		80									
	Lys	Phe	Asp	Gln	Met	Leu	Leu	Thr	Ala	Gln	Asn	Leu	Pro	Ala	Ser	Tyr
				85						90					95	
5	Asn	Tyr	Cys	Arg	Leu	Val	Ser	Arg	Ser	Leu	Thr	Val	Arg	Ser	Ser	Thr
				100					105					110		
10	Leu	Pro	Gly	Gly	Val	Tyr	Ala	Leu	Asn	Gly	Thr	Ile	Asn	Ala	Val	Thr
			115					120					125			
	Phe	Gln	Gly	Ser	Leu	Ser	Glu	Leu	Thr	Asp	Val	Ser	Tyr	Asn	Gly	Leu
	130					135						140				
15	Met	Ser	Ala	Thr	Ala	Asn	Ile	Asn	Asp	Lys	Ile	Gly	Asn	Val	Leu	Val
	145					150					155				160	
	Gly	Glu	Gly	Val	Thr	Val	Leu	Ser	Leu	Pro	Thr	Ser	Tyr	Asp	Leu	Gly
				165						170				175		
20	Tyr	Val	Arg	Leu	Gly	Asp	Pro	Ile	Pro	Ala	Ile	Gly	Leu	Asp	Pro	Lys
				180					185					190		
25	Met	Val	Ala	Thr	Cys	Asp	Ser	Ser	Asp	Arg	Pro	Arg	Val	Tyr	Thr	Ile
		195						200					205			
	Thr	Ala	Ala	Asp	Asp	Tyr	Gln	Phe	Ser	Ser	Gln	Tyr	Gln	Pro	Gly	Gly
	210						215					220				
30	Val	Thr	Ile	Thr	Leu	Phe	Ser	Ala	Asn	Ile	Asp	Ala	Ile	Thr	Ser	Leu
	225					230					235				240	
	Ser	Val	Gly	Gly	Glu	Leu	Val	Phe	Gln	Thr	Ser	Val	His	Gly	Leu	Val
				245					250					255		
35	Leu	Gly	Ala	Thr	Ile	Tyr	Leu	Ile	Gly	Phe	Asp	Gly	Thr	Thr	Val	Ile
			260						265					270		
40	Thr	Arg	Ala	Val	Ala	Ala	Asn	Asn	Gly	Leu	Thr	Thr	Gly	Thr	Asp	Asn
		275						280					285			
	Leu	Met	Pro	Phe	Asn	Leu	Val	Ile	Pro	Thr	Asn	Glu	Ile	Thr	Gln	Pro
	290						295					300				
45	Ile	Thr	Ser	Ile	Lys	Leu	Glu	Ile	Val	Thr	Ser	Lys	Ser	Gly	Gly	Gln
	305					310					315				320	
	Ala	Gly	Asp	Gln	Met	Ser	Trp	Ser	Ala	Arg	Gly	Ser	Leu	Ala	Val	Thr

	325	330	335
	Ile His Gly Gly Asn Tyr Pro Gly Ala Leu Arg Pro Val Thr Leu Val		
	340	345	350
5	Ala Tyr Glu Arg Val Ala Thr Gly Ser Val Val Thr Val Ala Gly Val		
	355	360	365
10	Ser Asn Phe Glu Leu Ile Pro Asn Pro Glu Leu Ala Lys Asn Leu Val		
	370	375	380
	Thr Glu Tyr Gly Arg Phe Asp Pro Gly Ala Met Asn Tyr Thr Lys Leu		
	385	390	395 400
15	Ile Leu Ser Glu Arg Asp Arg Leu Gly Ile Lys Thr Val Trp Pro Thr		
	405	410	415
	Arg Glu Tyr Thr Asp Phe Arg Glu Tyr Phe Met Glu Val Ala Asp Leu		
	420	425	430
20	Asn Ser Pro Leu Lys Ile Ala Gly Ala Phe Gly Phe Lys Asp Ile Ile		
	435	440	445
	Arg Ala Ile Arg Arg Ile Ala Val Pro Val Val Ser Thr Leu Phe Pro		
25	450	455	460
	Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val Asp Tyr Leu		
	465	470	475 480
30	Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg Ala Ala Ser		
	485	490	495
	Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu Thr Leu Ala		
	500	505	510
35	Ala Asp Lys Gly Tyr Glu Val Val Ala Asn Leu Phe Gln Val Pro Gln		
	515	520	525
	Asn Pro Val Val Asp Gly Ile Leu Ala Ser Pro Gly Val Leu Arg Gly		
40	530	535	540
	Ala His Asn Leu Asp Cys Val Leu Arg Glu Gly Ala Thr Leu Phe Pro		
	545	550	555 560
45	Val Val Ile Thr Thr Val Glu Asp Ala Met Thr Pro Lys Ala Leu Asn		
	565	570	575
	Ser Lys Met Phe Ala Val Ile Glu Gly Val Arg Glu Asp Leu Gln Pro		

	580		585		590
	Pro Ser Gln Arg Gly Ser Phe Ile Arg Thr Leu Ser Gly His Arg Val				
	595		600		605
5	Tyr Gly Tyr Ala Pro Asp Gly Val Leu Pro Leu Glu Thr Gly Arg Asp				
	610		615		620
	Tyr Thr Val Val Pro Ile Asp Asp Val Trp Asp Asp Ser Ile Met Leu				
10	625		630		640
	Ser Lys Asp Pro Ile Pro Pro Ile Val Gly Asn Ser Gly Asn Leu Ala				
		645		650	655
15	Ile Ala Tyr Met Asp Val Phe Arg Pro Lys Val Pro Ile His Val Ala				
		660		665	670
	Met Thr Gly Ala Leu Asn Ala Cys Gly Glu Ile Glu Lys Val Ser Phe				
		675		680	685
20	Arg Ser Thr Lys Leu Ala Thr Ala His Arg Leu Gly Leu Arg Leu Ala				
		690		695	700
	Gly Pro Gly Ala Phe Asp Val Asn Thr Gly Pro Asn Trp Ala Thr Phe				
25	705		710		720
	Ile Lys Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr				
		725		730	735
30	Leu Asn Leu Pro Tyr Leu Pro Pro Asn Ala Gly Arg Gln Tyr His Leu				
		740		745	750
	Ala Met Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Ser Ala				
		755		760	765
35	Val Arg Ala Met Glu Ala Ala Ala Asn Val Asp Pro Leu Phe Gln Ser				
		770		775	780
	Ala Leu Ser Val Phe Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp				
40	785		790		800
	Met Ala Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Arg Asn				
		805		810	815
45	Phe Leu Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys				
		820		825	830
	Tyr Gly Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu				

	835		840		845
	Glu Ala Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr				
	850		855		860
5	Met Gly Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His				
	865		870		875 880
	Arg Gly Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg Glu				
10		885		890	895
	Ile Pro Asp Pro Asn Glu Asp Tyr Leu Asp Tyr Val His Ala Glu Lys				
		900		905	910
15	Ser Arg Leu Ala Ser Glu Glu Gln Ile Leu Arg Ala Ala Thr Ser Ile				
		915		920	925
	Tyr Gly Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu				
20		930		935	940
	Val Ala Lys Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu				
		945		950	955 960
	Gln Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn				
25		965		970	975
	Pro Arg Arg Ala Leu Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Thr				
		980		985	990
30	Gln Arg Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp				
		995		1000	1005
	Glu Asp Leu Glu				
35		1010			

(2) INFORMATION FOR SEQ ID NO: 7:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- 45 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:97..531

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGATACGATC GGTCTGACCC CGGGGGAGTC ACCCGGGGAC AGGCCGTCAA GGCCTTGTTTC 60

10 CAGGATGGGA CTCCTCCTTC TACAACGCTA TCATTC GAA GTT AGT TGA GAT CTG 114
 Glu Val Ser * Asp Leu
 1 5

15 ACA AAC GAT CGC AGC GAT GAC AAA CCT GCA AGA TCA AAC CCA ACA GAT 162
 Thr Asn Asp Arg Ser Asp Asp Lys Pro Ala Arg Ser Asn Pro Thr Asp
 10 15 20

20 (2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2827 base pairs

(B) TYPE: nucleic acid

25 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

30

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:112..2745

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GGATACGATG GGTCTGACCC TCTGGGAGTC ACGAATTAAC GTGGCTACTA GGGGCGATAC 60

40 CCGCCGCTGG CTGCCACGTT AGTGGCTCCT CTTCTTGATG ATTCTGCCAC C ATG AGT 117
 Met Ser
 1

45 GAC ATT TTC AAC AGT CCA CAG GCG CGA AGC ACG ATC TCA GCA GCG TTC 165
 Asp Ile Phe Asn Ser Pro Gln Ala Arg Ser Thr Ile Ser Ala Ala Phe
 5 10 15

GGC ATA AAG CCT ACT GCT GGA CAA GAC GTG GAA GAA CTC TTG ATC CCT 213

	Gly	Ile	Lys	Pro	Thr	Ala	Gly	Gln	Asp	Val	Glu	Glu	Leu	Leu	Ile	Pro	
	20						25					30					
5	AAA	GTT	TGG	GTG	CCA	CCT	GAG	GAT	CCG	CTT	GCC	AGC	CCT	AGT	CGA	CTG	261
	Lys	Val	Trp	Val	Pro	Pro	Glu	Asp	Pro	Leu	Ala	Ser	Pro	Ser	Arg	Leu	
	35					40					45					50	
10	GCA	AAG	TTC	CTC	AGA	GAG	AAC	GGC	TAC	AAA	GTT	TTG	CAG	CCG	CGG	TCT	309
	Ala	Lys	Phe	Leu	Arg	Glu	Asn	Gly	Tyr	Lys	Val	Leu	Gln	Pro	Arg	Ser	
				55					60						65		
15	CTG	CCC	GAG	AAT	GAG	GAG	TAT	GAG	ACC	GAC	CAA	ATA	CTC	CCA	GAC	TTA	357
	Leu	Pro	Glu	Asn	Glu	Glu	Tyr	Glu	Thr	Asp	Gln	Ile	Leu	Pro	Asp	Leu	
				70				75						80			
20	GCA	TGG	ATG	CGA	CAG	ATA	GAA	GGG	GCT	GTT	TTA	AAA	CCC	ACT	CTA	TCT	405
	Ala	Trp	Met	Arg	Gln	Ile	Glu	Gly	Ala	Val	Leu	Lys	Pro	Thr	Leu	Ser	
		85						90					95				
25	CTC	CCT	ATT	GGA	GAT	CAG	GAG	TAC	TTC	CCA	AAG	TAC	TAC	CCA	ACA	CAT	453
	Leu	Pro	Ile	Gly	Asp	Gln	Glu	Tyr	Phe	Pro	Lys	Tyr	Tyr	Pro	Thr	His	
		100					105					110					
30	CGC	CCT	AGC	AAG	GAG	AAG	CCC	AAT	GCG	TAC	CCG	CCA	GAC	ATC	GCA	CTA	501
	Arg	Pro	Ser	Lys	Glu	Lys	Pro	Asn	Ala	Tyr	Pro	Pro	Asp	Ile	Ala	Leu	
		115					120				125					130	
35	CTC	AAG	CAG	ATG	ATT	TAC	CTG	TTT	CTC	CAG	GTT	CCA	GAG	GCC	AAC	GAG	549
	Leu	Lys	Gln	Met	Ile	Tyr	Leu	Phe	Leu	Gln	Val	Pro	Glu	Ala	Asn	Glu	
				135					140						145		
40	GGC	CTA	AAG	GAT	GAA	GTA	ACC	CTC	TTG	ACC	CAA	AAC	ATA	AGG	GAC	AAG	597
	Gly	Leu	Lys	Asp	Glu	Val	Thr	Leu	Leu	Thr	Gln	Asn	Ile	Arg	Asp	Lys	
				150					155					160			
45	GCC	TAT	GGA	AGT	GGG	ACC	TAC	ATG	GGA	CAA	GCA	ACT	CGA	CTT	GTG	GCC	645
	Ala	Tyr	Gly	Ser	Gly	Thr	Tyr	Met	Gly	Gln	Ala	Thr	Arg	Leu	Val	Ala	
		165						170					175				
50	ATG	AAG	GAG	GTC	GCC	ACT	GGA	AGA	AAC	CCA	AAC	AAG	GAT	CCT	CTA	AAG	693
	Met	Lys	Glu	Val	Ala	Thr	Gly	Arg	Asn	Pro	Asn	Lys	Asp	Pro	Leu	Lys	
		180						185					190				
55	CTT	GGG	TAC	ACT	TTT	GAG	AGC	ATC	GCG	CAG	CTA	CTT	GAC	ATC	ACA	CTA	741
	Leu	Gly	Tyr	Thr	Phe	Glu	Ser	Ile	Ala	Gln	Leu	Leu	Asp	Ile	Thr	Leu	
		195					200					205				210	
60	CCG	GTA	GGC	CCA	CCC	GGT	GAG	GAT	GAC	AAG	CCC	TGG	GTG	CCA	CTC	ACA	789

	Pro	Val	Gly	Pro	Pro	Gly	Glu	Asp	Asp	Lys	Pro	Trp	Val	Pro	Leu	Thr	
					215					220					225		
5	AGA	GTG	CCG	TCA	CGG	ATG	TTG	GTG	CTG	ACG	GGA	GAC	GTA	GAT	GGC	GAC	837
	Arg	Val	Pro	Ser	Arg	Met	Leu	Val	Leu	Thr	Gly	Asp	Val	Asp	Gly	Asp	
				230					235					240			
10	TTT	GAG	GTT	GAA	GAT	TAC	CTT	CCC	AAA	ATC	AAC	CTC	AAG	TCA	TCA	AGT	885
	Phe	Glu	Val	Glu	Asp	Tyr	Leu	Pro	Lys	Ile	Asn	Leu	Lys	Ser	Ser	Ser	
		245					250					255					
15	GGA	CTA	CCA	TAT	GTA	GGT	CGC	ACC	AAA	GGA	GAG	ACA	ATT	GGC	GAG	ATG	933
	Gly	Leu	Pro	Tyr	Val	Gly	Arg	Thr	Lys	Gly	Glu	Thr	Ile	Gly	Glu	Met	
		260				265				270							
20	ATA	GCT	ATA	TCA	AAC	CAG	TTT	CTC	AGA	GAG	CTA	TCA	ACA	CTG	TTG	AAG	981
	Ile	Ala	Ile	Ser	Asn	Gln	Phe	Leu	Arg	Glu	Leu	Ser	Thr	Leu	Leu	Lys	
	275				280				285				290				
25	CAA	GGT	GCA	GGG	ACA	AAG	GGG	TCA	AAC	AAG	AAG	AAG	CTA	CTC	AGC	ATG	1029
	Gln	Gly	Ala	Gly	Thr	Lys	Gly	Ser	Asn	Lys	Lys	Lys	Leu	Leu	Ser	Met	
				295				300					305				
30	TTA	AGT	GAC	TAT	TGG	TAC	TTA	TCA	TGC	GGG	CTT	TTG	TTT	CCA	AAG	GCT	1077
	Leu	Ser	Asp	Tyr	Trp	Tyr	Leu	Ser	Cys	Gly	Leu	Leu	Phe	Pro	Lys	Ala	
			310					315					320				
35	GAA	AGG	TAC	GAC	AAA	AGT	ACA	TGG	CTC	ACC	AAG	ACC	CGG	AAC	ATA	TGG	1125
	Glu	Arg	Tyr	Asp	Lys	Ser	Thr	Trp	Leu	Thr	Lys	Thr	Arg	Asn	Ile	Trp	
		325					330					335					
40	TCA	GCT	CCA	TCC	CCA	ACA	CAC	CTC	ATG	ATC	TCC	ATG	ATC	ACC	TGG	CCC	1173
	Ser	Ala	Pro	Ser	Pro	Thr	His	Leu	Met	Ile	Ser	Met	Ile	Thr	Trp	Pro	
		340				345					350						
45	GTG	ATG	TCC	AAC	AGC	CCA	AAT	AAC	GTG	TTG	AAC	ATT	GAA	GGG	TGT	CCA	1221
	Val	Met	Ser	Asn	Ser	Pro	Asn	Asn	Val	Leu	Asn	Ile	Glu	Gly	Cys	Pro	
	355				360				365				370				
50	TCA	CTC	TAC	AAA	TTC	AAC	CCG	TTC	AGA	GGA	GGG	TTG	AAC	AGG	ATC	GTC	1269
	Ser	Leu	Tyr	Lys	Phe	Asn	Pro	Phe	Arg	Gly	Gly	Leu	Asn	Arg	Ile	Val	
				375				380					385				
55	GAG	TGG	ATA	TTG	GCC	CCG	GAA	GAA	CCC	AAG	GCT	CTT	GTA	TAT	GCG	GAC	1317
	Glu	Trp	Ile	Leu	Ala	Pro	Glu	Glu	Pro	Lys	Ala	Leu	Val	Tyr	Ala	Asp	
			390				395					400					
60	AAC	ATA	TAC	ATT	GTC	CAC	TCA	AAC	ACG	TGG	TAC	TCA	ATT	GAC	CTA	GAG	1365

	Asn	Ile	Tyr	Ile	Val	His	Ser	Asn	Thr	Trp	Tyr	Ser	Ile	Asp	Leu	Glu	
	405							410						415			
5	AAG	GGT	GAG	GCA	AAC	TGC	ACT	CGC	CAA	CAC	ATG	CAA	GCC	GCA	ATG	TAC	1413
	Lys	Gly	Glu	Ala	Asn	Cys	Thr	Arg	Gln	His	Met	Gln	Ala	Ala	Met	Tyr	
	420						425					430					
10	TAC	ATA	CTC	ACC	AGA	GGG	TGG	TCA	GAC	AAC	GGC	GAC	CCA	ATG	TTC	AAT	1461
	Tyr	Ile	Leu	Thr	Arg	Gly	Trp	Ser	Asp	Asn	Gly	Asp	Pro	Met	Phe	Asn	
	435					440					445				450		
15	CAA	ACA	TGG	GCC	ACC	TTT	GCC	ATG	AAC	ATT	GCC	CCT	GCT	CTA	GTG	GTG	1509
	Gln	Thr	Trp	Ala	Thr	Phe	Ala	Met	Asn	Ile	Ala	Pro	Ala	Leu	Val	Val	
				455						460					465		
	GAC	TCA	TCG	TGC	CTG	ATA	ATG	AAC	CTG	CAA	ATT	AAG	ACC	TAT	GGT	CAA	1557
	Asp	Ser	Ser	Cys	Leu	Ile	Met	Asn	Leu	Gln	Ile	Lys	Thr	Tyr	Gly	Gln	
				470						475					480		
20	GGC	AGC	GGG	AAT	GCA	GCC	ACG	TTC	ATC	AAC	AAC	CAC	CTC	TTG	AGC	ACG	1605
	Gly	Ser	Gly	Asn	Ala	Ala	Thr	Phe	Ile	Asn	Asn	His	Leu	Leu	Ser	Thr	
	485						490					495					
25	CTA	GTG	CTT	GAC	CAG	TGG	AAC	TTG	ATG	AGA	CAG	CCC	AGA	CCA	GAC	AGC	1653
	Leu	Val	Leu	Asp	Gln	Trp	Asn	Leu	Met	Arg	Gln	Pro	Arg	Pro	Asp	Ser	
	500						505					510					
30	GAG	GAG	TTC	AAA	TCA	ATT	GAG	GAC	AAG	CTA	GGT	ATC	AAC	TTT	AAG	ATT	1701
	Glu	Glu	Phe	Lys	Ser	Ile	Glu	Asp	Lys	Leu	Gly	Ile	Asn	Phe	Lys	Ile	
	515					520					525				530		
35	GAG	AGG	TCC	ATT	GAT	GAT	ATC	AGG	GGC	AAG	CTG	AGA	CAG	CTT	GTC	CTC	1749
	Glu	Arg	Ser	Ile	Asp	Asp	Ile	Arg	Gly	Lys	Leu	Arg	Gln	Leu	Val	Leu	
				535						540					545		
	CTT	GCA	CAA	CCA	GGG	TAC	CTG	AGT	GGG	GGG	GTT	GAA	CCA	GAA	CAA	TCC	1797
	Leu	Ala	Gln	Pro	Gly	Tyr	Leu	Ser	Gly	Gly	Val	Glu	Pro	Glu	Gln	Ser	
				550						555					560		
40	AGC	CCA	ACT	GTT	GAG	CTT	GAC	CTA	CTA	GGG	TGG	TCA	GCT	ACA	TAC	AGC	1845
	Ser	Pro	Thr	Val	Glu	Leu	Asp	Leu	Leu	Gly	Trp	Ser	Ala	Thr	Tyr	Ser	
	565						570					575					
45	AAA	GAT	CTC	GGG	ATC	TAT	GTG	CCG	GTG	CTT	GAC	AAG	GAA	CGC	CTA	TTT	1893
	Lys	Asp	Leu	Gly	Ile	Tyr	Val	Pro	Val	Leu	Asp	Lys	Glu	Arg	Leu	Phe	
	580					585					590						
	TGT	TCT	GCT	GCG	TAT	CCC	AAG	GGA	GTA	GAG	AAC	AAG	AGT	CTC	AAG	TCC	1941

	Cys	Ser	Ala	Ala	Tyr	Pro	Lys	Gly	Val	Glu	Asn	Lys	Ser	Leu	Lys	Ser	
	595					600					605					610	
5	AAA	GTC	GGG	ATC	GAG	CAG	GCA	TAC	AAG	GTA	GTC	AGG	TAT	GAG	GCG	TTG	1989
	Lys	Val	Gly	Ile	Glu	Gln	Ala	Tyr	Lys	Val	Val	Arg	Tyr	Glu	Ala	Leu	
					615					620					625		
10	AGG	TTG	GTA	GGT	GGT	TGG	AAC	TAC	CCA	CTC	CTG	AAC	AAA	GCC	TGC	AAG	2037
	Arg	Leu	Val	Gly	Gly	Trp	Asn	Tyr	Pro	Leu	Leu	Asn	Lys	Ala	Cys	Lys	
				630					635					640			
15	AAT	AAC	GCA	GGC	GCC	GCT	CGG	CGG	CAT	CTG	GAG	GCC	AAG	GGG	TTC	CCA	2085
	Asn	Asn	Ala	Gly	Ala	Ala	Arg	Arg	His	Leu	Glu	Ala	Lys	Gly	Phe	Pro	
			645					650					655				
	CTC	GAC	GAG	TTC	CTA	GCC	GAG	TGG	TCT	GAG	CTG	TCA	GAG	TTC	GGT	GAG	2133
	Leu	Asp	Glu	Phe	Leu	Ala	Glu	Trp	Ser	Glu	Leu	Ser	Glu	Phe	Gly	Glu	
		660					665					670					
20	GCC	TTC	GAA	GGC	TTC	AAT	ATC	AAG	CTG	ACC	GTA	ACA	TCT	GAG	AGC	CTA	2181
	Ala	Phe	Glu	Gly	Phe	Asn	Ile	Lys	Leu	Thr	Val	Thr	Ser	Glu	Ser	Leu	
		675				680					685					690	
25	GCC	GAA	CTG	AAC	AAG	CCA	GTA	CCC	CCC	AAG	CCC	CCA	AAT	GTC	AAC	AGA	2229
	Ala	Glu	Leu	Asn	Lys	Pro	Val	Pro	Pro	Lys	Pro	Pro	Asn	Val	Asn	Arg	
					695					700					705		
30	CCA	GTC	AAC	ACT	GGG	GGA	CTC	AAG	GCA	GTC	AGC	AAC	GCC	CTC	AAG	ACC	2277
	Pro	Val	Asn	Thr	Gly	Gly	Leu	Lys	Ala	Val	Ser	Asn	Ala	Leu	Lys	Thr	
				710					715					720			
35	GGT	CGG	TAC	AGG	AAC	GAA	GCC	GGA	CTG	AGT	GGT	CTC	GTC	CTT	CTA	GCC	2325
	Gly	Arg	Tyr	Arg	Asn	Glu	Ala	Gly	Leu	Ser	Gly	Leu	Val	Leu	Leu	Ala	
			725					730					735				
40	ACA	GCA	AGA	AGC	CGT	CTG	CAA	GAT	GCA	GTT	AAG	GCC	AAG	GCA	GAA	GCC	2373
	Thr	Ala	Arg	Ser	Arg	Leu	Gln	Asp	Ala	Val	Lys	Ala	Lys	Ala	Glu	Ala	
			740				745				750						
45	GAG	AAA	CTC	CAC	AAG	TCC	AAG	CCA	GAC	GAC	CCC	GAT	GCA	GAC	TGG	TTC	2421
	Glu	Lys	Leu	His	Lys	Ser	Lys	Pro	Asp	Asp	Pro	Asp	Ala	Asp	Trp	Phe	
		755				760					765					770	
50	GAA	AGA	TCA	GAA	ACT	CTG	TCA	GAC	CTT	CTG	GAG	AAA	GCC	GAC	ATC	GCC	2469
	Glu	Arg	Ser	Glu	Thr	Leu	Ser	Asp	Leu	Leu	Glu	Lys	Ala	Asp	Ile	Ala	
					775					780					785		
55	AGC	AAG	GTC	GCC	CAC	TCA	GCA	CTC	GTG	GAA	ACA	AGC	GAC	GCC	CTT	GAA	2517

	Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala Leu Glu	
	790 795 800	
5	GCA GTT CAG TCG ACT TCC GTG TAC ACC CCC AAG TAC CCA GAA GTC AAG Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu Val Lys	2565
	805 810 815	
10	AAC CCA CAG ACC GCC TCC AAC CCC GTT GTT GGG CTC CAC CTG CCC GCC Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu Pro Ala	2613
	820 825 830	
15	AAG AGA GCC ACC GGT GTC CAG GCC GCT CTT CTC GGA GCA GGA ACG AGC Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly Thr Ser	2661
	835 840 845 850	
20	AGA CCA ATG GGG ATG GAG GCC CCA ACA CGG TCC AAG AAC GCC GTG AAA Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala Val Lys	2709
	855 860 865	
25	ATG GCC AAA CGG CGG CAA CGC CAA AAG GAG AGC CGC TAACAGCCAT Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg	2755
	870 875	
30	GATGGGAACC ACTCAAGAAG AGGACACTAA TCCCAGACCC CGTATCCCCG GCCTTCGCCT	2815
	GCGGGGGCCC CC	2827